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PATENT APPLICATION

MYCOBACTERIAL *RpoB* SEQUENCES

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**MYCOBACTERIAL *RpoB* SEQUENCES****STATEMENT OF GOVERNMENT INTEREST**

[0001] The work described in this application was supported in part by grant number 1R43a140400 by the NIAID. The Government may have certain rights in this invention.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0002] This application derives priority from USSN 60/080,616, filed April 3, 1998, and incorporated by reference. Applications USSN 08/797,812, filed February 7, 1997, now US Patent 6,228,575; USSN 60/011,339, filed Feb. February 8, 1996; USSN 60/012,631, filed March 1 1996; USSN 08/629,031, filed April 8, 1996, now abandoned; and 60/017,765, filed 15 May 15, 1996 are directed to related subject matter. These applications are specifically incorporated by reference in their entirety for all purposes.

BACKGROUND OF THE INVENTIONField of the Invention

[0003] This invention is directed to polymorphisms in *rpoB* genes of mycobacteria and use of the same in the identification and characterization of microorganisms.

Background of the Invention

[0004] Multidrug resistance and human immunodeficiency virus (HIV-1) infections are factors which have had a profound impact on the tuberculosis problem. An increase in the frequency of *Mycobacterium tuberculosis* strains resistant to one or more anti-mycobacterial agents has been reported, Block, et al., (1994) JAMA 271:665-671. Immunocompromised HIV-1 infected patients not infected with *M. tuberculosis* are frequently infected with *M. avium* complex (MAC) or *M. avium-M. intracellulare* (MAI) complex. These mycobacteria species are often resistant to

the drugs used to treat *M. tuberculosis*. These factors have re-emphasized the importance for the accurate determination of drug sensitivities and mycobacteria species identification.

[0005] In HIV-1 infected patients, the correct diagnosis of the mycobacterial disease is essential since treatment of *M. tuberculosis* infections differs from that called for by other mycobacteria infections, Hoffner, S.E. (1994) *Eur. J. Clin. Microbiol. Inf. Dis.* **13**:937-941. Non-tuberculosis mycobacteria commonly associated with HIV-1 infections include *M. kansasii*, *M. xenopi*, *M. fortuitum*, *M. avium* and *M. intracellulare*, Wolinsky, E., (1992) *Clin. Infect. Dis.* **15**:1-12, Shafer, R.W. and Sierra, M.F. 1992 *Clin. Infect. Dis.* **15**:161-162. Additionally, 13% of new cases (HIV-1 infected and non-infected) of *M. tuberculosis* are resistant to one of the primary anti-tuberculosis drugs (isoniazid [INH], rifampin [RIF], streptomycin [STR], ethambutol [EMB] and pyrazinamide [PZA] and 3.2% are resistant to both RIF and INH, Block, et al., *JAMA* **271**:665-671, (1994). Consequently, mycobacterial species identification and the determination of drug resistance have become central concerns during the diagnosis of mycobacterial diseases.

[0006] Methods used to detect, and to identify *Mycobacterium* species vary considerably. For detection of *Mycobacterium tuberculosis*, microscopic examination of acid-fast stained smears and cultures are still the methods of choice in most microbiological clinical laboratories. However, culture of clinical samples is hampered by the slow growth of mycobacteria. A mean time of four weeks is required before sufficient growth is obtained to enable detection and possible identification. Recently, two more rapid methods for culture have been developed involving a radiometric, Stager, C.E. et al., (1991) *J. Clin. Microbiol.* **29**:154-157, and a biphasic (broth/agar) system Sewell, et al., (1993) *J. Clin. Microbiol.* **29**:2689-2472. Once grown, cultured mycobacteria can be analyzed by lipid composition, the use of species specific antibodies, species specific DNA or RNA probes and PCR-based sequence analysis of 16S rRNA gene (Schirm, et al. (1995) *J. Clin. Microbiol.* **33**:3221-3224; Kox, et al. (1995) *J. Clin. Microbiol.* **33**:3225-3233) and IS6110 specific repetitive sequence analysis (For a review see, e.g., Small et al., P.M. and van Embden, J.D.A. (1994) *Am. Society for Microbiology*, pp. 569-582). The analysis of 16S rRNA sequences (RNA and DNA) has been the most informative molecular approach to identify *Mycobacteria* species (Jonas, et al., *J. Clin. Microbiol.* **31**:2410-

2416 (1993)). However, to obtain drug sensitivity information for the same isolate, additional protocols (culture) or alternative gene analysis is necessary.

[0007] To determine drug sensitivity information, culture methods are still the protocols of choice. *Mycobacteria* are judged to be resistant to particular drugs by use of either the standard proportional plate method or minimal inhibitory concentration (MIC) method. However, given the inherent lengthy times required by culture methods, approaches to determine drug sensitivity based on molecular genetics have been recently developed.

[0008] Because resistance to RIF in *E. coli* strains was observed to arise as a result of mutations in the *rpoB* gene, Telenti, et al., id., identified a 69 base pair (bp) region of the *M. tuberculosis rpoB* gene as the locus where RIF resistant mutations were focused. Kapur, et al., (1995) *Arch. Pathol. Lab. Med.* 119:131-138, identified additional novel mutations in the *M. tuberculosis rpoB* gene which extended this core region to 81 bp. In a detailed review on antimicrobial agent resistance in mycobacteria, Musser (*Clin. Microbiol. Rev.*, 8:496-514 (1995)), summarized all the characterized mutations and their relative frequency of occurrence in this 81 bp region of *rpoB*. Missense mutations comprise 88% of all known mutations while insertions (3 or 6 bp) and deletions (3, 6 and 9 bp) account for 4% and 8% of the remaining mutations, respectively. Approximately 90% of all RIF resistant tuberculosis isolates have been shown to have mutations in this 81 bp region. The remaining 10% are thought possibly to involve genes other than *rpoB*.

[0009] For the above reasons, it would be desirable to have simpler methods which identify and characterize microorganisms, such as *Mycobacteria*, both at the phenotypic and genotypic level. This invention fulfills that and related needs.

SUMMARY OF THE INVENTION

[0010] In one aspect, the invention provides isolated nucleic acids comprising at least 25, 50, 75, 100, or 200 contiguous bases from an *rpoB* sequence shown in Table 1 (SEQ ID NOS: 1-181). Some nucleic acid comprise a complete sequence shown in Table 1.

[0011] The invention further provides a set of probes perfectly complementary to and spanning such nucleic acids, preferably spanning one of the complete sequences shown in Table 1 (SEQ ID NOS: 1-181).

[0012] The invention further provides methods of classifying mycobacteria. Some such methods entail providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria, determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid; comparing the determined sequence to at least one sequence shown in Table 1; and classifying the mycobacteria from the extent of similarity of the compared sequences. Preferably, at least 100 or 200 contiguous bases are determined from the target nucleic acid. Preferably, the determined sequence is compared with a plurality of sequences from Table 1, for example, 10, 20, 50 or all of the sequence from Table 1 (SEQ ID NOS: 1-181).

[0013] In other methods of classification, the identity of one or more bases in the target sequence at one or more positions corresponding to one or more of the highlighted positions in a sequence shown in Table 1 is determined. The identity of the one or more bases characterizing the species of mycobacteria that is present in the sample. In some methods, the identity of at least 10 bases in the target nucleic acid at positions corresponding to highlighted positions in a sequence shown in Table 1 is determined. In some methods, the identity of at least 20 bases in the target sequence at highlighted positions shown in Table 1 are identified. In some methods, at least 20 determined bases are compared with 20 bases occupying corresponding positions in each of at least ten sequences from Table 1.

[0014] In another aspect, the invention provides sequence-specific polynucleotide probes or primers that hybridizes to a segment of a mycobacterial rpoB sequence shown in Table 1 or its complement without hybridizing to the *M. tuberculosis* sequence designated ATCC9-Mtb in Table 1 or its complement, the segment including a highlighted nucleotide position shown in Table 1. In some such probes, a central position of the probe aligns with a highlighted nucleotide position shown in Table 1. In some such primers, the 3' end of the primer aligns with a highlighted nucleotide position shown in Table 1. Some probes and primers are between 10 and 50 bases long.

[0015] In another aspect, the invention provides a computer-readable storage medium for storing data for access by an application program being executed on a data processing system. Such a system comprises a data structure stored in the computer-readable storage medium. The data structure includes information resident in a database used by the application program and includes a plurality of records, each record comprising information identifying a polymorphism

or sequence shown in Table 1. Some records have a field identifying a base occupying a polymorphic site and a field identifying location of the polymorphic site. Some records record a contiguous segment of at least 50, 100, or 200 bases from an rpoB sequence shown in Table 1. Some storage medium comprise at least ten records each recording a contiguous segment of at least 50 bases from at least ten rpoB sequences shown in Table 1.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] Fig. 1: Computer that may be utilized to execute software embodiments of the present invention.

[0017] Fig. 2: A system block diagram of a typical computer system that may be used to execute software embodiments of the invention.

DEFINITIONS

[0018] A polynucleotide can be DNA or RNA, and single- or double-stranded. Polynucleotide can be naturally occurring or synthetic, and can be of any length. Preferred polynucleotide probes of the invention include contiguous segments of DNA, or their complements including any of the highlighted bases shown in Table 1. The segments are usually between 5 and 100 bases, and often between 5-10, 5-20, 10-20, 10-50, 20-50 or 20-100 bases. The highlighted site can occur within any position of the segment. Preferred polynucleotide probes are capable of binding in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991), and probes having nonnaturally occurring bases.

[0019] The term primer refers to a single-stranded polynucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions (*i.e.*, in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair

means a set of primers including a 5' upstream primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3', downstream primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

[0020] A cDNA or cRNA is derived from an RNA if it produced by a process in which the RNA serves as a template for production of the cDNA or cRNA.

[0021] Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5 x SSPE (750 mM NaCl, 50 mM Na Phosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridizations.

[0022] An isolated nucleic acid means an object species invention that is the predominant species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition). Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods).

[0023] For sequence comparison and homology determination, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0024] Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by visual inspection (*see generally*, Ausubel *et al.*, *infra*).

[0025] One example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, *J. Mol.*

Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, $M=5$, $N=-4$, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915).

[0026] In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul (1993) *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

[0027] The term “target nucleic acid” refers to a nucleic acid (often derived from a biological sample), to which the probe nucleic acid is designed to specifically hybridize. It is the presence or expression level of the target nucleic acid that is to be detected or quantified. The target nucleic acid has a sequence that is complementary to the nucleic acid sequence of the corresponding probe directed to the target. The term target nucleic acid may refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (e.g. gene or mRNA) whose expression level it is desired to detect. The difference in usage will be apparent from context.

[0028] “Subsequence” refers to a sequence of nucleic acids that comprise a part of a longer sequence of nucleic acids.

DETAILED DESCRIPTION

I. Mycobacterial Sequences of rpoB Genes

[0029] Table 1 shows a comparison of a substantial collection of mycobacterial strains of an about 700-nucleotide conserved region of an rpoB gene. The sequences shown in Table 1 are identified as follows: SEQ ID NOS: 1-56, respectively, are shown on pages 21, 25, 29, 33, 37, 41, 45, 49, 53, 57, 61 and 65; SEQ ID NOS: 57-112, respectively, are shown on pages 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62 and 65; SEQ ID NOS: 113-168, respectively, are shown on pages 23, 27, 31, 35, 39, 43, 47, 51, 55, 59, 63 and 66; SEQ ID NOS: 169-181, respectively, are shown on pages 24, 28, 32, 36, 40, 44, 52, 56, 60, 64 and 68. The first sequence, designated as a reference sequence, is from *M. tuberculosis*. Nucleotides are numbered consecutively starting from the first nucleotide of the reference sequences. Other sequences are from other strains of mycobacteria. For example, the sequences designated ATCC-av, M29, M30...M104 are from *M. avium*. Sequences designated from ATT-chelnew, M11, M13, and M17 are from *M. chelonae*. Sequences designated ATCC-for, M53, M55, M56, and M74 are from *M. fortuitum*, and so forth. Complete correspondence between strain designations and strain types is shown in Table 2. Nucleotides in a mycobacterial sequence are accorded the same number as the corresponding position of the reference sequence when the two are maximally aligned. Differences between a sequence and the reference sequences are shown in highlighted type. Many of the highlighted positions are common to all tested members of a species. Other highlighted positions vary

among different isolates in a species. Both types of variation can be useful in speciation analysis.

II. Analysis of Species Variations

A. Preparation of Samples

[0030] An *rpoB* sequence is isolated from a sample of an unknown mycobacteria being tested. Nucleic acids can be isolated from mycobacteria by standard methods as described in WO 97/29212 (incorporated by reference in its entirety for all purposes). The *rpoB* sequences to be analyzed can then be isolated and amplified by means of PCR. *See generally PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202 (each of which is incorporated by reference for all purposes). Primers for PCR preferably flank the regions of interest *rpoB* genes, although primers to internal sites can be used if it is intended to analyze only certain sites of potential species variation. Exemplary primers are described in WO 97/29212. If necessary, additional sequences flanking the sequences shown in Table 1 can be determined using probes based on the sequences in Table 1 to isolate full-length *rpoB* sequences from the appropriate mycobacterial species.

B. Detection of Species-Specific Variations in Target DNA

1. Sequence-Specific Probes

[0031] The design and use of sequence-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Sequence-specific probes can be designed that hybridize to a segment of target DNA in one isolate of mycobacteria that do not isolate to a corresponding isolate in another due to the presence of allelic or species variations in the respective segments from the two sequences. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the sequences. Some probes are designed to hybridize to a

segment of target DNA such that the site of potential sequence variation aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic and species variants.

[0032] Sequence-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple potential variations within the same target sequence.

2. Tiling Arrays

[0033] The bases occupying sites of potential variation can also be identified by hybridization to nucleic acid arrays, some example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). Such arrays contain a series of overlapping probes spanning a reference sequence. Any of the *rpoB* sequences shown in Table 1, or contiguous segments of, for example, at least 25, 50, 100 or 200 bases thereof, can serve as a reference sequence. WO 95/11995 also describes subarrays that are optimized for detection of a variant forms of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is a variant of the first reference sequence. The inclusion of a second group (or further groups) can be particular useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (*i.e.*, two or more mutations within 9 to 21 bases).

3. Sequence-Specific Primers

[0034] A sequence-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of a variant form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular variant form is present. A control is usually performed with a second pair of primers, one of which

shows a single base mismatch at the site of variation and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the primer aligned with the point of variation because this position is most destabilizing to elongation from the primer. *See, e.g.*, WO 93/22456.

4. Direct-Sequencing

[0035] The direct analysis of mycobacterial sequences can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)).

III. Methods of Use

[0036] The sequences and polymorphisms shown in Table 1 are useful for identifying the presence of mycobacteria in samples, and optionally, classifying the mycobacteria. The sample can be obtained from a patient or from a biological source, such as a food product.

[0037] The sequences shown in Table 1 can be used for design of sequence-specific probes or primers encompassing polymorphic sites as described above. These probes or primers can then be used to determine the base occupying a corresponding position in an *rpoB* sequence from an isolate in a sample under test. A base in one sequence corresponds with a base in another when the two bases occupy the same position when the two sequences are maximally aligned by one of the criteria described in Definitions.

[0038] Alternatively, the sequences shown in Table 1 can be used for design of tiling arrays in which one or more of the sequences serves as a reference sequence. At least one set of overlapping probes is designed spanning a segment of the reference sequence, as described in WO95/11995 or EP 717,113. Target sequences from samples under test can be hybridized to such arrays, optionally in combination with controls of known *rpoB* sequences. The hybridization pattern of a target sequence to such an array can be analyzed to determine the identity of bases at which the target sequence differs from the reference sequence, as described in WO 95/11995.

[0039] One or more of the above methods, or direct sequencing, can be used to identify the base occupying at least one and usually several (e.g., 5, 10, 15, 25, 50 or 100) sites of potential variation between the 16S RNA and/or rpoB gene in an unknown mycobacteria relative to bases occupying corresponding sites in one or more known strains of mycobacteria, such as those shown in Table 1. This analysis results in a profile of bases occupying particular sites that characterizes the mycobacterial strain under test. The profile is compared with the corresponding profiles of different mycobacterial isolates shown in e.g., Table 1. In general, the unknown mycobacterium isolate is characterized as being from the same mycobacterial species as the precharacterized isolate with which it shares the greatest similarity in base profile.

[0040] In some methods, the sequence of a contiguous segment of the rpoB target nucleic acid is determined in a sample under test for comparison with one or more of the sequences shown in Table 1. The mycobacteria is classified by the extent of similarity. For example, if a target nucleic acid shows greater sequence identity to rpoB sequences from one species than any other, the sample from which the target was obtained is typically classified as arising from that species.

[0041] Alternatively, an array of tiled probes based on a reference sequence shown in Table 1 can be used for identifying and characterizing mycobacterial sequences based on comparison of hybridization patterns. Such an array is hybridized to a 16S RNA or rpoB target sequence from a sample, and the hybridization pattern compared with the hybridization pattern of one or more control sequences. The hybridization patterns of control sequences can be historic controls, stored, for example, in a computer database, or can be contemporaneous controls performed at or near the same time as the hybridization to the target sequence. Optionally, hybridization of target and reference sequence can be performed simultaneously using different labels.

[0042] Method of classifying unknown mycobacterial isolate by matching the hybridization pattern of a target sequence with those of control sequences from characterized species are described in more detail in WO 97/29212 (incorporated by reference in its entirety for all purposes). In an idealized case, the detection of a particular hybridization pattern in an isolate characterizes that isolate as belonging to a particular species. This can occur when the hybridization pattern detected in the isolate is uniquely associated with a specific species. More frequently however, such an unique one-to-one correspondence is not present. Instead, the hybridization pattern observed in an isolate does not bear a unique correspondence with a

previously characterized species. However, the hybridization pattern detected is associated with a probability of the organism being screened belonging to a particular species (or not) or carrying a particular phenotypic trait (or not). As a result, analysis of an increasing number of polymorphic sites in an isolate, allows one to classify the isolated with an increasing level of confidence. Algorithms can be used to derive such composite probabilities from the comparison of multiple polymorphic forms between an isolate and references. Typically, the mathematical algorithm makes a call of the identity of the species and assign a confidence level to that call. One can determine the confidence level (>90%, >95% etc.) that one desires and the algorithm will analyze the hybridization pattern and either provide an identification or not. Occasionally, the call is that the sample may be one of two, three or more species, in which case a specific identification is not be possible. However, one of the strengths of this technique is that the rapid screening made possible by the chip-based hybridization allows one to continuously expand a database of patterns ultimately to enable the identification of species previously unidentifiable due to lack of sufficient information.

IV. Modified Polypeptides and Gene Sequences

[0043] The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in Table 1. Some nucleic acid encode full-length variant forms of proteins. Variant proteins have the prototypical amino acid sequences of encoded by nucleic acid sequence shown in Table 1 (read so as to be in-frame with the full-length coding sequence of which it is a component).

[0044] Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

[0045] The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, *e.g.*, mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

[0046] The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

[0047] In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

[0048] Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986).

Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

[0049] The invention further provides kits comprising at least one sequence-specific probe as described above. Often, the kits contain one or more pairs of sequence-specific probes hybridizing to different forms of a polymorphism. In some kits, the sequence-specific probes are provided immobilized to a substrate. For example, the same substrate can comprise sequence-specific probes for detecting at least 10, 100 or all of the variations shown in Table 1. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

VI. Computer Databases

[0050] Fig. 1 illustrates an example of a computer system that can be used to store records relating to polymorphisms of the invention and perform algorithms comparing polymorphic profiles and to classify species. Fig. 2 shows a computer system 100 which includes a monitor 102, screen 104, cabinet 106, keyboard 108, and mouse 110. Mouse 110 may have one or more buttons such as mouse buttons 112. Cabinet 106 houses a CD-ROM drive 114, a system memory and a hard drive (see Fig. 2) which can be utilized to store and retrieve software programs incorporating code that implements the present invention, data for use with the present invention, and the like. Although a CD-ROM 116 is shown as an exemplary computer readable storage medium, other computer readable storage media including floppy disks, tape, flash memory, system memory, and hard drives may be utilized. Cabinet 106 also houses familiar computer components such as a central processor, system memory, hard disk, and the like.

[0051] Fig. 2 shows a system block diagram of computer system 100 that may be used to execute software embodiments of the present invention. As in Fig. 1, computer system 100 includes monitor 102 and keyboard 108. Computer system 100 further includes subsystems such as a central processor 102, system memory 120, I/O controller 122, display adapter 124, removable disk 126 (e.g., CD-ROM drive), fixed disk 128 (e.g., hard drive), network interface 130, and speaker 132. Other computer systems suitable for use with the present invention may include additional or fewer subsystems. For example, another computer system can include more than one processor 102 (i.e., a multi-processor system) or a cache memory.

[0052] Arrows such as 134 represent the system bus architecture of computer system 100. However, these arrows are illustrative of any interconnection scheme serving to link the subsystems. For example, a local bus can be utilized to connect the central processor to the system memory and display adapter. Computer system 100 shown in Fig. 1 is but an example of a computer system suitable for use with the present invention.

[0053] The computer stores records relating to the polymorphisms of the record. Some such records record a polymorphism by reference to the position of a polymorphic site and the identity of base(s) occupying that site in one or more species. Some databases include records for at least ten polymorphic sites in at least ten of the sequences shown in Table 1. Some databases include records for all of the polymorphic sites in at least one of the sequences shown in Table 1. Some databases includes records for at least 100, 1000, or 2000 polymorphic sites shown in Table 1. Some databases include records for all of the polymorphic sites shown in Table 1.

[0054] The foregoing invention has been described in some detail by way of illustration and example, for purposes of clarity and understanding. It will be obvious to one of skill in the art that changes and modifications may be practiced within the scope of the appended claims. Therefore, it is to be understood that the above description is intended to be illustrative and not restrictive. The scope of the invention should, therefore, be determined not with reference to the above description, but should instead be determined with reference to the following appended claims, along with the full scope of equivalents to which such claims are entitled.

[0055] All patents, patent applications and publications cited in this application are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual patent, patent application or publication were so individually denoted.

Table 1
BASE NOS 1-60

ATCC9-Mtb.txt	SEQ ID NO 1	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T GAT CAACA T CCG GCG CGG
MY621.txt	SEQ ID NO 2	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
Atcc1-av.txt	SEQ ID NO 3	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M29.txt	SEQ ID NO 4	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M30.txt	SEQ ID NO 5	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M31.txt	SEQ ID NO 6	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M32.txt	SEQ ID NO 7	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M33.txt	SEQ ID NO 8	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M34.txt	SEQ ID NO 9	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M48-new.txt	SEQ ID NO 10	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M49.txt	SEQ ID NO 11	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M64 (Mav2).txt	SEQ ID NO 12	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M65 (Mav3).txt	SEQ ID NO 13	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M67 (Mav5).txt	SEQ ID NO 14	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M69 (Mav7).txt	SEQ ID NO 15	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M71 (Mav9).txt	SEQ ID NO 16	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M91.txt	SEQ ID NO 17	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M94.txt	SEQ ID NO 18	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M95.txt	SEQ ID NO 19	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M96.txt	SEQ ID NO 20	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M100.txt	SEQ ID NO 21	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M101.txt	SEQ ID NO 22	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M102.txt	SEQ ID NO 23	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M104.txt	SEQ ID NO 24	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M105.txt	SEQ ID NO 25	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M106.txt	SEQ ID NO 26	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M111.txt	SEQ ID NO 27	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M76.txt	SEQ ID NO 28	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
MY451.txt	SEQ ID NO 29	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
ATCC2-chelnew.txt	SEQ ID NO 30	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M10.txt	SEQ ID NO 31	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M11-662.txt	SEQ ID NO 32	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M12.txt	SEQ ID NO 33	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M13 2_662.txt	SEQ ID NO 34	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M14.txt	SEQ ID NO 35	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M15.txt	SEQ ID NO 36	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M16.txt	SEQ ID NO 37	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M17 2_662.txt	SEQ ID NO 38	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M50.txt	SEQ ID NO 39	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M51.txt	SEQ ID NO 40	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M115.txt	SEQ ID NO 41	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M116.txt	SEQ ID NO 42	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M119.txt	SEQ ID NO 43	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
MY109.txt	SEQ ID NO 44	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
MY200.txt	SEQ ID NO 45	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
MY207.txt	SEQ ID NO 46	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
MY209.txt	SEQ ID NO 47	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M122.txt	SEQ ID NO 48	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M123.txt	SEQ ID NO 49	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M124.txt	SEQ ID NO 50	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
Atcc3-for.txt	SEQ ID NO 51	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M53.txt	SEQ ID NO 52	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M54.txt	SEQ ID NO 53	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M55.txt	SEQ ID NO 54	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M56.txt	SEQ ID NO 55	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG
M74 (Mav12).txt	SEQ ID NO 56	CCCA GGACGT GGA GGC GAT CACA CGC AGA CGT T CCG GCG CGG

Table 1
BASE NOS 1-60

M77. txt	SEQ ID NO 57	CCCA GGACGT GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M118. txt	SEQ ID NO 58	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY221. txt	SEQ ID NO 59	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY223. txt	SEQ ID NO 60	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY225. txt	SEQ ID NO 61	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY341. txt	SEQ ID NO 62	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY715. txt	SEQ ID NO 63	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY470. txt	SEQ ID NO 64	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
Atcc4-go. txt	SEQ ID NO 65	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
ATCC4-0-Gord. txt	SEQ ID NO 66	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M79(lz). txt	SEQ ID NO 67	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M79(jd). txt	SEQ ID NO 68	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M80(lg). txt	SEQ ID NO 69	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M81(l1). txt	SEQ ID NO 70	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M82(rm). txt	SEQ ID NO 71	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M83(mb). txt	SEQ ID NO 72	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M84(ow). txt	SEQ ID NO 73	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M85(lb). txt	SEQ ID NO 74	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M86(rb). txt	SEQ ID NO 75	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M87(wm). txt	SEQ ID NO 76	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M90(gordDB). txt	SEQ ID NO 77	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
m126. txt	SEQ ID NO 78	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M128. txt	SEQ ID NO 79	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
My103. txt	SEQ ID NO 80	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY475. txt	SEQ ID NO 81	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY476. txt	SEQ ID NO 82	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY830. txt	SEQ ID NO 83	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
Atcc5-int. txt	SEQ ID NO 84	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
ATCC5-Oint. txt	SEQ ID NO 85	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M18. txt	SEQ ID NO 86	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M19. txt	SEQ ID NO 87	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M20. txt	SEQ ID NO 88	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M21. txt	SEQ ID NO 89	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M22. txt	SEQ ID NO 90	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M23. txt	SEQ ID NO 91	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M24. txt	SEQ ID NO 92	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M25. txt	SEQ ID NO 93	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M26. txt	SEQ ID NO 94	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M27. txt	SEQ ID NO 95	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M28. txt	SEQ ID NO 96	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M107. txt	SEQ ID NO 97	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY107. txt	SEQ ID NO 98	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY112. txt	SEQ ID NO 99	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
MY312. txt	SEQ ID NO 100	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
Atcc6-kan. txt	SEQ ID NO 101	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
ATCC6-OKan. txt	SEQ ID NO 102	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M1. txt	SEQ ID NO 103	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M2. txt	SEQ ID NO 104	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M3. txt	SEQ ID NO 105	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M4. txt	SEQ ID NO 106	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M6. txt	SEQ ID NO 107	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M7. txt	SEQ ID NO 108	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M9. txt	SEQ ID NO 109	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M57. txt	SEQ ID NO 110	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M58. txt	SEQ ID NO 111	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG
M59. txt	SEQ ID NO 112	GGAGGCGAT CACACCGCAGAC	CTGATCAACATCCG	CGGTGGTGGCGG

Table 1

[illegible]

Table 1
BASE NOS 1-60

M38.txt	SEQ ID NO 169	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M39.txt	SEQ ID NO 170	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M40.txt	SEQ ID NO 171	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M41.txt	SEQ ID NO 172	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M42.txt	SEQ ID NO 173	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M43.txt	SEQ ID NO 174	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M44.txt	SEQ ID NO 175	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M45.txt	SEQ ID NO 176	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M46.txt	SEQ ID NO 177	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M47.txt	SEQ ID NO 178	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M68 (Mav6).txt	SEQ ID NO 179	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M89.txt	SEQ ID NO 180	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
M66 (Mav4).txt	SEQ ID NO 181	CCAGGACGTTGGAGGCGGATCACACCGCAGAC	TTGATCAACATCCG	CCGTGGTGGCGG
		102030405060		

Table 1
BASE NOS 61-120

ATCC9-Mcb.txt	SEQ.ID NO 1	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY621.txt	SEQ.ID NO 2	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
Atcc1-av.txt	SEQ.ID NO 3	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M29.txt	SEQ.ID NO 4	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M30.txt	SEQ.ID NO 5	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M31.txt	SEQ.ID NO 6	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M32.txt	SEQ.ID NO 7	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M33.txt	SEQ.ID NO 8	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M34.txt	SEQ.ID NO 9	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M48-new.txt	SEQ.ID NO 10	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M49.txt	SEQ.ID NO 11	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M64 (Mav2).txt	SEQ.ID NO 12	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M65 (Mav3).txt	SEQ.ID NO 13	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M67 (Mav5).txt	SEQ.ID NO 14	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M69 (Mav7).txt	SEQ.ID NO 15	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M71 (Mav9).txt	SEQ.ID NO 16	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M91.txt	SEQ.ID NO 17	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M94.txt	SEQ.ID NO 18	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M95.txt	SEQ.ID NO 19	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M96.txt	SEQ.ID NO 20	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M100.txt	SEQ.ID NO 21	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M101.txt	SEQ.ID NO 22	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M102.txt	SEQ.ID NO 23	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M104.txt	SEQ.ID NO 24	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M105.txt	SEQ.ID NO 25	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M106.txt	SEQ.ID NO 26	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY111.txt	SEQ.ID NO 27	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M76.txt	SEQ.ID NO 28	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY451.txt	SEQ.ID NO 29	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
ATCC2-chelnew.txt	SEQ.ID NO 30	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M10.txt	SEQ.ID NO 31	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M11-662.txt	SEQ.ID NO 32	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M12.txt	SEQ.ID NO 33	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M13_2_662.txt	SEQ.ID NO 34	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M14.txt	SEQ.ID NO 35	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M15.txt	SEQ.ID NO 36	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M16.txt	SEQ.ID NO 37	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M17_2_662.txt	SEQ.ID NO 38	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M50.txt	SEQ.ID NO 39	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M51.txt	SEQ.ID NO 40	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M115.txt	SEQ.ID NO 41	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M116.txt	SEQ.ID NO 42	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M119.txt	SEQ.ID NO 43	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M109.txt	SEQ.ID NO 44	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY200.txt	SEQ.ID NO 45	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY207.txt	SEQ.ID NO 46	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
MY209.txt	SEQ.ID NO 47	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M122.txt	SEQ.ID NO 48	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M123.txt	SEQ.ID NO 49	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M124.txt	SEQ.ID NO 50	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
Atcc3-for.txt	SEQ.ID NO 51	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M53.txt	SEQ.ID NO 52	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M54.txt	SEQ.ID NO 53	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M55.txt	SEQ.ID NO 54	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M56.txt	SEQ.ID NO 55	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC
M74 (Mav12).txt	SEQ.ID NO 56	CGATCAAGGAGTTCCTCGGCAACGAGCCAGCTGAGCCAAATTCATGGACCAAGAACAAACCCGC

Table 1
BASE NOS 61-120

M77.txt	SEQ.ID.NO.57	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M118.txt	SEQ.ID.NO.58	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M121.txt	SEQ.ID.NO.59	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M223.txt	SEQ.ID.NO.60	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M225.txt	SEQ.ID.NO.61	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M341.txt	SEQ.ID.NO.62	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M715.txt	SEQ.ID.NO.63	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M470.txt	SEQ.ID.NO.64	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
Atcc4-go.txt	SEQ.ID.NO.65	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
ATCC4-0-Gord.txt	SEQ.ID.NO.66	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M78(1z).txt	SEQ.ID.NO.67	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M79(jd).txt	SEQ.ID.NO.68	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M80(1g).txt	SEQ.ID.NO.69	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M81(1l).txt	SEQ.ID.NO.70	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M82(1m).txt	SEQ.ID.NO.71	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M83(mb).txt	SEQ.ID.NO.72	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M84(ow).txt	SEQ.ID.NO.73	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M85(1b).txt	SEQ.ID.NO.74	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M86(1b).txt	SEQ.ID.NO.75	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M87(wn).txt	SEQ.ID.NO.76	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M90(gordDB).txt	SEQ.ID.NO.77	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
m126.txt	SEQ.ID.NO.78	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M128.txt	SEQ.ID.NO.79	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
My103.txt	SEQ.ID.NO.80	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY475.txt	SEQ.ID.NO.81	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY476.txt	SEQ.ID.NO.82	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY830.txt	SEQ.ID.NO.83	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
Atcc5-int.txt	SEQ.ID.NO.84	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
ATCC5-0-int.txt	SEQ.ID.NO.85	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M18.txt	SEQ.ID.NO.86	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M19.txt	SEQ.ID.NO.87	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M20.txt	SEQ.ID.NO.88	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M21.txt	SEQ.ID.NO.89	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M22.txt	SEQ.ID.NO.90	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M23.txt	SEQ.ID.NO.91	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M24.txt	SEQ.ID.NO.92	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M25.txt	SEQ.ID.NO.93	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M26.txt	SEQ.ID.NO.94	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M27.txt	SEQ.ID.NO.95	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M28.txt	SEQ.ID.NO.96	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M107.txt	SEQ.ID.NO.97	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY107.txt	SEQ.ID.NO.98	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY112.txt	SEQ.ID.NO.99	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
MY312.txt	SEQ.ID.NO.100	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
Atcc6-kan.txt	SEQ.ID.NO.101	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
ATCC6-0kan.txt	SEQ.ID.NO.102	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M1.txt	SEQ.ID.NO.103	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M2.txt	SEQ.ID.NO.104	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M3.txt	SEQ.ID.NO.105	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M4.txt	SEQ.ID.NO.106	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M6.txt	SEQ.ID.NO.107	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M7.txt	SEQ.ID.NO.108	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M9.txt	SEQ.ID.NO.109	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M57.txt	SEQ.ID.NO.110	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M58.txt	SEQ.ID.NO.111	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC
M59.txt	SEQ.ID.NO.112	CGATCAAGGAGTTCTTCGGCACCCAGCCAGCTGTTCATGGACCAAGAACACCCGC

Table 1
BASE NOS 61-120

M38. txt	SEQ ID NO 169	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	1	CGA	TTTCATGGA	CAGAACAAACCCGC		
M39. txt	SEQ ID NO 170	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	2	CGA	TTTCATGGA	CAGAACAAACCCGC		
M40. txt	SEQ ID NO 171	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	3	CGA	TTTCATGGA	CAGAACAAACCCGC		
M41. txt	SEQ ID NO 172	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	4	CGA	TTTCATGGA	CAGAACAAACCCGC		
M42. txt	SEQ ID NO 173	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	5	CGA	TTTCATGGA	CAGAACAAACCCGC		
M43. txt	SEQ ID NO 174	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	6	CGA	TTTCATGGA	CAGAACAAACCCGC		
M44. txt	SEQ ID NO 175	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	7	CGA	TTTCATGGA	CAGAACAAACCCGC		
M45. txt	SEQ ID NO 176	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	8	CGA	TTTCATGGA	CAGAACAAACCCGC		
M46. txt	SEQ ID NO 177	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	9	CGA	TTTCATGGA	CAGAACAAACCCGC		
M47. txt	SEQ ID NO 178	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	10	CGA	TTTCATGGA	CAGAACAAACCCGC		
M48 (Mav6). txt	SEQ ID NO 179	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	11	CGA	TTTCATGGA	CAGAACAAACCCGC		
M49. txt	SEQ ID NO 180	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	12	CGA	TTTCATGGA	CAGAACAAACCCGC		
M56 (Mav4). txt	SEQ ID NO 181	CGATCAAGGAGTTCCTTCGGCACCGAGCCAGCT	13	CGA	TTTCATGGA	CAGAACAAACCCGC		
			70	80	90	100	110	120

Table 1
BASE NOS 121-180

M77.txt	SEQ ID NO 57	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M118.txt	SEQ ID NO 58	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M221.txt	SEQ ID NO 59	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M223.txt	SEQ ID NO 60	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M225.txt	SEQ ID NO 61	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My341.txt	SEQ ID NO 62	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My715.txt	SEQ ID NO 63	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
MY470.txt	SEQ ID NO 64	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
Atcc6-go.txt	SEQ ID NO 65	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
ATCC4-0-Gord.txt	SEQ ID NO 66	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M78(1z).txt	SEQ ID NO 67	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M79(jd).txt	SEQ ID NO 68	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M80(lg).txt	SEQ ID NO 69	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M81(11).txt	SEQ ID NO 70	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M82(em).txt	SEQ ID NO 71	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M83(mb).txt	SEQ ID NO 72	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M84(ow).txt	SEQ ID NO 73	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M85(lb).txt	SEQ ID NO 74	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M86(xb).txt	SEQ ID NO 75	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M87(wm).txt	SEQ ID NO 76	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M90(gordDB).txt	SEQ ID NO 77	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
m126.txt	SEQ ID NO 78	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M128.txt	SEQ ID NO 79	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My103.txt	SEQ ID NO 80	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My475.txt	SEQ ID NO 81	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My476.txt	SEQ ID NO 82	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My830.txt	SEQ ID NO 83	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
Atcc5-int.txt	SEQ ID NO 84	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
ATCC5-0int.txt	SEQ ID NO 85	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M18.txt	SEQ ID NO 86	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M19.txt	SEQ ID NO 87	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M20.txt	SEQ ID NO 88	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M21.txt	SEQ ID NO 89	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M22.txt	SEQ ID NO 90	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M23.txt	SEQ ID NO 91	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M24.txt	SEQ ID NO 92	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M25.txt	SEQ ID NO 93	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M26.txt	SEQ ID NO 94	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M27.txt	SEQ ID NO 95	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M28.txt	SEQ ID NO 96	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My107.txt	SEQ ID NO 97	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My112.txt	SEQ ID NO 98	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
My312.txt	SEQ ID NO 99	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
Atcc6-han.txt	SEQ ID NO 100	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
ATCC6-0kan.txt	SEQ ID NO 101	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M1.txt	SEQ ID NO 102	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M2.txt	SEQ ID NO 103	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M3.txt	SEQ ID NO 104	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M4.txt	SEQ ID NO 105	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M6.txt	SEQ ID NO 106	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M7.txt	SEQ ID NO 107	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M9.txt	SEQ ID NO 108	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M57.txt	SEQ ID NO 109	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M58.txt	SEQ ID NO 110	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
M59.txt	SEQ ID NO 111	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG
	SEQ ID NO 112	TGT CCGGG	TGACCCACAAAGCG	CTGTGTGGCGGCTGGG	CCCCGGCGGCTGTGTCT	CGTG

Table 1
BASE NOS 121-180

M38. txt	SEQ ID NO 169	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M39. txt	SEQ ID NO 170	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M40. txt	SEQ ID NO 171	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M41. txt	SEQ ID NO 172	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M42. txt	SEQ ID NO 173	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M43. txt	SEQ ID NO 174	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M44. txt	SEQ ID NO 175	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M45. txt	SEQ ID NO 176	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M46. txt	SEQ ID NO 177	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M47. txt	SEQ ID NO 178	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M68 (Mav6). txt	SEQ ID NO 179	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M89. txt	SEQ ID NO 180	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG
M66 (Mav4). txt	SEQ ID NO 181	TGT CGGGGG	TACCCACACAAGCGG	CGGCT	TCGGCGGCT	GGT	CC	GGCGGCTCTGTCT	CGG

Table 1
BASE NOS 181-240

ATCC9-Mtb.txt	SEQ.ID.NO.1	AGCGTGGCGGGCTGGAGGTCGCGGACGTGCAACCGTGCACCGTTCGCACTACGGCCGGATGTGCCCGA
MY621.txt	SEQ.ID.NO.2	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
Atcc1-av.txt	SEQ.ID.NO.3	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M29.txt	SEQ.ID.NO.4	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M30.txt	SEQ.ID.NO.5	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M31.txt	SEQ.ID.NO.6	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M32.txt	SEQ.ID.NO.7	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M33.txt	SEQ.ID.NO.8	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M34.txt	SEQ.ID.NO.9	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M48-new.txt	SEQ.ID.NO.10	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M49.txt	SEQ.ID.NO.11	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M64(Mav2).txt	SEQ.ID.NO.12	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M65(Mav3).txt	SEQ.ID.NO.13	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M67(Mav5).txt	SEQ.ID.NO.14	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M69(Mav7).txt	SEQ.ID.NO.15	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M71(Mav9).txt	SEQ.ID.NO.16	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M91.txt	SEQ.ID.NO.17	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M94.txt	SEQ.ID.NO.18	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M95.txt	SEQ.ID.NO.19	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M96.txt	SEQ.ID.NO.20	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M100.txt	SEQ.ID.NO.21	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M101.txt	SEQ.ID.NO.22	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M102.txt	SEQ.ID.NO.23	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M104.txt	SEQ.ID.NO.24	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M105.txt	SEQ.ID.NO.25	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M106.txt	SEQ.ID.NO.26	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY111.txt	SEQ.ID.NO.27	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M76.txt	SEQ.ID.NO.28	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY451.txt	SEQ.ID.NO.29	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
ATCC2-chelnew.txt	SEQ.ID.NO.30	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M10.txt	SEQ.ID.NO.31	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M11-662.txt	SEQ.ID.NO.32	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M12.txt	SEQ.ID.NO.33	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M13_2_662.txt	SEQ.ID.NO.34	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M14.txt	SEQ.ID.NO.35	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M15.txt	SEQ.ID.NO.36	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M16.txt	SEQ.ID.NO.37	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M17_2_662.txt	SEQ.ID.NO.38	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M50.txt	SEQ.ID.NO.39	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M51.txt	SEQ.ID.NO.40	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M115.txt	SEQ.ID.NO.41	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M116.txt	SEQ.ID.NO.42	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M119.txt	SEQ.ID.NO.43	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY109.txt	SEQ.ID.NO.44	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY200.txt	SEQ.ID.NO.45	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY207.txt	SEQ.ID.NO.46	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
MY209.txt	SEQ.ID.NO.47	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M122.txt	SEQ.ID.NO.48	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M123.txt	SEQ.ID.NO.49	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M124.txt	SEQ.ID.NO.50	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
Atcc3-for.txt	SEQ.ID.NO.51	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M53.txt	SEQ.ID.NO.52	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M54.txt	SEQ.ID.NO.53	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M55.txt	SEQ.ID.NO.54	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M56.txt	SEQ.ID.NO.55	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA
M74(Mav12).txt	SEQ.ID.NO.56	AGCGGGCGGGCTGGAGGTCGCGGACGTGCAACCGTTCGCACTACGGCCGGATGTGCCCGA

Table 1

M77.txt	SEQ.ID.NO.57	AGCGTCCCGGCTGAGGTCGCGGACGTGCACCTCGACCTACGGCCCGATGTGCCCGG
M118.txt	SEQ.ID.NO.58	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M221.txt	SEQ.ID.NO.59	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M223.txt	SEQ.ID.NO.60	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M225.txt	SEQ.ID.NO.61	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M341.txt	SEQ.ID.NO.62	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M715.txt	SEQ.ID.NO.63	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M470.txt	SEQ.ID.NO.64	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
Atcc4-go.txt	SEQ.ID.NO.65	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
ATCC4-0-Gord.txt	SEQ.ID.NO.66	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M78(1z).txt	SEQ.ID.NO.67	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M79(jd).txt	SEQ.ID.NO.68	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M80(lg).txt	SEQ.ID.NO.69	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M81(1l).txt	SEQ.ID.NO.70	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M82(ze).txt	SEQ.ID.NO.71	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M83(mb).txt	SEQ.ID.NO.72	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M84(ow).txt	SEQ.ID.NO.73	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M85(1b).txt	SEQ.ID.NO.74	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M86(zb).txt	SEQ.ID.NO.75	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M87(wn).txt	SEQ.ID.NO.76	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M90(gordDB).txt	SEQ.ID.NO.77	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
m126.txt	SEQ.ID.NO.78	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M128.txt	SEQ.ID.NO.79	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My103.txt	SEQ.ID.NO.80	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My475.txt	SEQ.ID.NO.81	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My476.txt	SEQ.ID.NO.82	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My830.txt	SEQ.ID.NO.83	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
Atcc5-int.txt	SEQ.ID.NO.84	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
ATCC5-0int.txt	SEQ.ID.NO.85	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M18.txt	SEQ.ID.NO.86	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M19.txt	SEQ.ID.NO.87	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M20.txt	SEQ.ID.NO.88	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M21.txt	SEQ.ID.NO.89	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M22.txt	SEQ.ID.NO.90	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M23.txt	SEQ.ID.NO.91	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M24.txt	SEQ.ID.NO.92	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M25.txt	SEQ.ID.NO.93	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M26.txt	SEQ.ID.NO.94	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M27.txt	SEQ.ID.NO.95	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M28.txt	SEQ.ID.NO.96	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M107.txt	SEQ.ID.NO.97	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My107.txt	SEQ.ID.NO.98	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My112.txt	SEQ.ID.NO.99	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
My312.txt	SEQ.ID.NO.100	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
Atcc6-kan.txt	SEQ.ID.NO.101	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
ATCC6-0kan.txt	SEQ.ID.NO.102	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M1.txt	SEQ.ID.NO.103	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M2.txt	SEQ.ID.NO.104	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M3.txt	SEQ.ID.NO.105	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M4.txt	SEQ.ID.NO.106	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M6.txt	SEQ.ID.NO.107	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M7.txt	SEQ.ID.NO.108	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M9.txt	SEQ.ID.NO.109	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M57.txt	SEQ.ID.NO.110	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M58.txt	SEQ.ID.NO.111	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG
M59.txt	SEQ.ID.NO.112	AGCGTGCCCGGCTTGAAGTCCGCGACGTGCACCTACGGCCCGATGTGCCCGG

Table 1
BASE NOS 181-240

M38.txt	SEQ ID NO 169	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	240
M39.txt	SEQ ID NO 170	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M40.txt	SEQ ID NO 171	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M41.txt	SEQ ID NO 172	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M42.txt	SEQ ID NO 173	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M43.txt	SEQ ID NO 174	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M44.txt	SEQ ID NO 175	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M45.txt	SEQ ID NO 176	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M46.txt	SEQ ID NO 177	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M47.txt	SEQ ID NO 178	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M68 (Mav6).txt	SEQ ID NO 179	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M89.txt	SEQ ID NO 180	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	
M66 (Mav4).txt	SEQ ID NO 181	AGCGG	GCCGGGGCTGGAGG	GTCCG	GACGTGCAC	CG	CACTACGGCCGGATGTGCCCGA	

Table 1

SEQ ID NO 1	ATCC9-Mtb.txt
SEQ ID NO 2	MY621.txt
SEQ ID NO 3	Atcc1-av.txt
SEQ ID NO 4	M29.txt
SEQ ID NO 5	M30.txt
SEQ ID NO 6	M31.txt
SEQ ID NO 7	M32.txt
SEQ ID NO 8	M33.txt
SEQ ID NO 9	M34.txt
SEQ ID NO 10	M48-new.txt
SEQ ID NO 11	M49.txt
SEQ ID NO 12	M64 (Mav2).txt
SEQ ID NO 13	M65 (Mav3).txt
SEQ ID NO 14	M67 (Mav5).txt
SEQ ID NO 15	M69 (Mav7).txt
SEQ ID NO 16	M71 (Mav9).txt
SEQ ID NO 17	M91.txt
SEQ ID NO 18	M94.txt
SEQ ID NO 19	M95.txt
SEQ ID NO 20	M96.txt
SEQ ID NO 21	M100.txt
SEQ ID NO 22	M101.txt
SEQ ID NO 23	M102.txt
SEQ ID NO 24	M104.txt
SEQ ID NO 25	M105.txt
SEQ ID NO 26	M106.txt
SEQ ID NO 27	MY111.txt
SEQ ID NO 28	M76.txt
SEQ ID NO 29	MY451.txt
SEQ ID NO 30	ATCC2-chelnew.txt
SEQ ID NO 31	M10.txt
SEQ ID NO 32	M11-662.txt
SEQ ID NO 33	M12.txt
SEQ ID NO 34	M13-2_662.txt
SEQ ID NO 35	M14.txt
SEQ ID NO 36	M15.txt
SEQ ID NO 37	M16.txt
SEQ ID NO 38	M17_2_662.txt
SEQ ID NO 39	M50.txt
SEQ ID NO 40	M51.txt
SEQ ID NO 41	M115.txt
SEQ ID NO 42	M116.txt
SEQ ID NO 43	M119.txt
SEQ ID NO 44	MY109.txt
SEQ ID NO 45	MY200.txt
SEQ ID NO 46	MY207.txt
SEQ ID NO 47	MY209.txt
SEQ ID NO 48	M122.txt
SEQ ID NO 49	M123.txt
SEQ ID NO 50	M124.txt
SEQ ID NO 51	Atcc3-for.txt
SEQ ID NO 52	M53.txt
SEQ ID NO 53	M54.txt
SEQ ID NO 54	M55.txt
SEQ ID NO 55	M56.txt
SEQ ID NO 56	M74 (Mav12).txt

[illegible]

Table 1
BASE NOS 241-300

M38. txt	SEQ ID NO 169	T	C	G	A	A	C	C	C	C	G	A	G	G	G	C	C	A	A	C	A	T	C	G	G	T	T	T	G	A	T	C	G	G	G	C	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G	T	C	G	G	T	G
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Table 1
BASE NOS 301-360

M38.txt	SEQ ID NO 169	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M39.txt	SEQ ID NO 170	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M40.txt	SEQ ID NO 171	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M41.txt	SEQ ID NO 172	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M42.txt	SEQ ID NO 173	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M43.txt	SEQ ID NO 174	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M44.txt	SEQ ID NO 175	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M45.txt	SEQ ID NO 176	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M46.txt	SEQ ID NO 177	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M47.txt	SEQ ID NO 178	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M48 (Nav6).txt	SEQ ID NO 179	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M49.txt	SEQ ID NO 180	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
M56 (Nav4).txt	SEQ ID NO 181	TCAACCCCGT	ACGGGTTCAT	TGA	ACGCC	TACCGCAAGGTGGT	ACGGCGTGGT	ACGGCGTGGT	CG
		310	320	330	340	350	360		

SEQ ID NO 1	ATCC9-Mlb.txt	ACGAGATCTCGTATGCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 2	MY621.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 3	ATC9-av.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 4	M29.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 5	M30.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 6	M31.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 7	M32.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 8	M33.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 9	M434.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 10	M48-new.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 11	M49.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 12	M66 (Mav2) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 13	M65 (Mav3) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 14	M67 (Mav5) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 15	M69 (Mav7) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 16	M71 (Mav9) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 17	M91.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 18	M94.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 19	M95.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 20	M96.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 21	M100.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 22	M101.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 23	M102.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 24	M104.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 25	M105.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 26	M106.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 27	M111.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 28	M76.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 29	M451.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 30	M7CC2-chelnew.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 31	M10.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 32	M11-662.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 33	M12.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 34	M13 2_662.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 35	M14.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 36	M15.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 37	M16.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 38	M17 2_662.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 39	M50.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 40	M51.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 41	M15.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 42	M16.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 43	M19.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 44	M109.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 46	M200.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 47	M207.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 48	M123.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 49	M122.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 50	M124.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 51	Atcc3-for.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 52	M53.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 53	M54.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 54	M55.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 55	M56.txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA
SEQ ID NO 56	M74 (Mav12) .txt	ACGAGATCTTACCTGACCGCCGACGAGGAGGACCGCCACCGTGGTGGCCACAGGGCCAA

Table 1
BASE NOS 361-420

SEQ ID NO 169	M38. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 170	M39. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 171	M40. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 172	M41. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 173	M42. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 174	M43. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 175	M44. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 176	M45. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 177	M46. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 178	M47. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 179	M68(Mav6). txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 180	M89. txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
SEQ ID NO 181	M66(Mav4). txt	ACGAGATCGTGTACCTGACCGCCGACGAGGAGGACCGCCCA	GTGGTGGC	CAGGCCAACT			
		370	380	390	400	410	420

[illegible]

Table 1
BASE NOS 421-480

M177.txt	SEQ ID NO 57	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M118.txt	SEQ ID NO 58	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY221.txt	SEQ ID NO 59	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY223.txt	SEQ ID NO 60	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY225.txt	SEQ ID NO 61	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
My341.txt	SEQ ID NO 62	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
My715.txt	SEQ ID NO 63	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY470.txt	SEQ ID NO 64	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
Atcc4-go.txt	SEQ ID NO 65	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
ATCC4-0-Gord.txt	SEQ ID NO 66	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M78(1z).txt	SEQ ID NO 67	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M79(1d).txt	SEQ ID NO 68	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M80(1g).txt	SEQ ID NO 69	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M81(11).txt	SEQ ID NO 70	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M82(1m).txt	SEQ ID NO 71	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M83(1nb).txt	SEQ ID NO 72	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M84(1ow).txt	SEQ ID NO 73	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M85(1b).txt	SEQ ID NO 74	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M86(1xb).txt	SEQ ID NO 75	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M87(1wn).txt	SEQ ID NO 76	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M90(gordDB).txt	SEQ ID NO 77	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
m126.txt	SEQ ID NO 78	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M128.txt	SEQ ID NO 79	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
My103.txt	SEQ ID NO 80	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY475.txt	SEQ ID NO 81	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY476.txt	SEQ ID NO 82	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY830.txt	SEQ ID NO 83	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
Atcc5-int.txt	SEQ ID NO 84	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
ATCC5-0-int.txt	SEQ ID NO 85	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M18.txt	SEQ ID NO 86	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M19.txt	SEQ ID NO 87	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M20.txt	SEQ ID NO 88	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M21.txt	SEQ ID NO 89	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M22.txt	SEQ ID NO 90	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M23.txt	SEQ ID NO 91	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M24.txt	SEQ ID NO 92	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M25.txt	SEQ ID NO 93	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M26.txt	SEQ ID NO 94	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M27.txt	SEQ ID NO 95	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M28.txt	SEQ ID NO 96	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M107.txt	SEQ ID NO 97	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY107.txt	SEQ ID NO 98	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY112.txt	SEQ ID NO 99	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
MY312.txt	SEQ ID NO 100	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
Atcc6-kan.txt	SEQ ID NO 101	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
ATCC6-0kan.txt	SEQ ID NO 102	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M1.txt	SEQ ID NO 103	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M2.txt	SEQ ID NO 104	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M3.txt	SEQ ID NO 105	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M4.txt	SEQ ID NO 106	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M6.txt	SEQ ID NO 107	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M7.txt	SEQ ID NO 108	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M9.txt	SEQ ID NO 109	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M57.txt	SEQ ID NO 110	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M58.txt	SEQ ID NO 111	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC
M59.txt	SEQ ID NO 112	CGCCGATC	GAACCGGACCGGTCGCTTCA	CGAGGCGAGGCGCGGTGATGGTCC

Table 1

4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 10

Table 1

[illegible]

Table 1
BASE NOS 481-540

ATCC9-Mtb.txt	SEQ.ID.NO.1	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY621.txt	SEQ.ID.NO.2	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
Atcc1-av.txt	SEQ.ID.NO.3	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M29.txt	SEQ.ID.NO.4	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M30.txt	SEQ.ID.NO.5	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M31.txt	SEQ.ID.NO.6	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M32.txt	SEQ.ID.NO.7	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M33.txt	SEQ.ID.NO.8	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M34.txt	SEQ.ID.NO.9	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M48-new.txt	SEQ.ID.NO.10	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M49.txt	SEQ.ID.NO.11	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M64(Mav2).txt	SEQ.ID.NO.12	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M65(Mav3).txt	SEQ.ID.NO.13	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M67(Mav5).txt	SEQ.ID.NO.14	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M69(Mav7).txt	SEQ.ID.NO.15	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M71(Mav9).txt	SEQ.ID.NO.16	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M91.txt	SEQ.ID.NO.17	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M94.txt	SEQ.ID.NO.18	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M95.txt	SEQ.ID.NO.19	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M96.txt	SEQ.ID.NO.20	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M100.txt	SEQ.ID.NO.21	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M101.txt	SEQ.ID.NO.22	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M102.txt	SEQ.ID.NO.23	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M104.txt	SEQ.ID.NO.24	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M105.txt	SEQ.ID.NO.25	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M106.txt	SEQ.ID.NO.26	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY111.txt	SEQ.ID.NO.27	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M76.txt	SEQ.ID.NO.28	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY451.txt	SEQ.ID.NO.29	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
ATCC2-chelnew.txt	SEQ.ID.NO.30	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M10.txt	SEQ.ID.NO.31	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M11-662.txt	SEQ.ID.NO.32	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M12.txt	SEQ.ID.NO.33	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M13-2_662.txt	SEQ.ID.NO.34	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M14.txt	SEQ.ID.NO.35	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M15.txt	SEQ.ID.NO.36	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M16.txt	SEQ.ID.NO.37	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M17-2_662.txt	SEQ.ID.NO.38	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M50.txt	SEQ.ID.NO.39	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M51.txt	SEQ.ID.NO.40	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M115.txt	SEQ.ID.NO.41	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M116.txt	SEQ.ID.NO.42	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M119.txt	SEQ.ID.NO.43	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY109.txt	SEQ.ID.NO.44	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY200.txt	SEQ.ID.NO.45	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY207.txt	SEQ.ID.NO.46	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
MY209.txt	SEQ.ID.NO.47	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M122.txt	SEQ.ID.NO.48	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M123.txt	SEQ.ID.NO.49	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M124.txt	SEQ.ID.NO.50	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
Atcc3-for.txt	SEQ.ID.NO.51	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M53.txt	SEQ.ID.NO.52	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M54.txt	SEQ.ID.NO.53	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M55.txt	SEQ.ID.NO.54	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M56.txt	SEQ.ID.NO.55	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC
M74(Mav12).txt	SEQ.ID.NO.56	GCCGCAAGGCGGGCGAGGTTGGAGTACGTGCCCCCTCGTCTGAGGGTGGACTACATGGACGTC

Table 1
BASE NOS 481-540

M77.txt	SEQ ID NO 57	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M118.txt	SEQ ID NO 58	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY221.txt	SEQ ID NO 59	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY223.txt	SEQ ID NO 60	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY225.txt	SEQ ID NO 61	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY341.txt	SEQ ID NO 62	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY715.txt	SEQ ID NO 63	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY470.txt	SEQ ID NO 64	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
Atcc4-go.txt	SEQ ID NO 65	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
ATCC4-0-Gord.tx	SEQ ID NO 66	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M78(1x).txt	SEQ ID NO 67	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M79(jd).txt	SEQ ID NO 68	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M80(1g).txt	SEQ ID NO 69	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M81(1l).txt	SEQ ID NO 70	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M82(xm).txt	SEQ ID NO 71	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M83(mb).txt	SEQ ID NO 72	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M84(ow).txt	SEQ ID NO 73	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M85(1b).txt	SEQ ID NO 74	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M86(rz).txt	SEQ ID NO 75	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M87(wm).txt	SEQ ID NO 76	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M90(gordDB).txt	SEQ ID NO 77	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
m126.txt	SEQ ID NO 78	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M128.txt	SEQ ID NO 79	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
My103.txt	SEQ ID NO 80	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY475.txt	SEQ ID NO 81	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY476.txt	SEQ ID NO 82	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY830.txt	SEQ ID NO 83	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
Atcc5-int.txt	SEQ ID NO 84	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
ATCC5-Dint.txt	SEQ ID NO 85	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M18.txt	SEQ ID NO 86	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M19.txt	SEQ ID NO 87	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M20.txt	SEQ ID NO 88	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M21.txt	SEQ ID NO 89	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M22.txt	SEQ ID NO 90	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M23.txt	SEQ ID NO 91	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M24.txt	SEQ ID NO 92	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M25.txt	SEQ ID NO 93	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M26.txt	SEQ ID NO 94	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M27.txt	SEQ ID NO 95	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M28.txt	SEQ ID NO 96	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M107.txt	SEQ ID NO 97	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY107.txt	SEQ ID NO 98	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY112.txt	SEQ ID NO 99	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
MY312.txt	SEQ ID NO 100	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
Atcc6-kan.txt	SEQ ID NO 101	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
ATCC6-OKan.txt	SEQ ID NO 102	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M1.txt	SEQ ID NO 103	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M2.txt	SEQ ID NO 104	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M3.txt	SEQ ID NO 105	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M4.txt	SEQ ID NO 106	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M6.txt	SEQ ID NO 107	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M7.txt	SEQ ID NO 108	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M9.txt	SEQ ID NO 109	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M57.txt	SEQ ID NO 110	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M58.txt	SEQ ID NO 111	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT
M59.txt	SEQ ID NO 112	GCCG	AAAGG	GGCG	AGGT	GGAG	ACGT	GGCG	CGTC	GA	GT	GACT	ACAT	GGAC	GTCT

BASE NOS 481-540

[illegible]

Table 1
BASE NOS 481-540

M38. txt	SEQ ID NO 169	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	530
M39. txt	SEQ ID NO 170	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	540
M40. txt	SEQ ID NO 171	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M41. txt	SEQ ID NO 172	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M42. txt	SEQ ID NO 173	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M43. txt	SEQ ID NO 174	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M44. txt	SEQ ID NO 175	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M45. txt	SEQ ID NO 176	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M46. txt	SEQ ID NO 177	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M47. txt	SEQ ID NO 178	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M48 (Mav6). txt	SEQ ID NO 179	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M49. txt	SEQ ID NO 180	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	
M56 (Mav4). txt	SEQ ID NO 181	GCCGCCAAGGGG	GGGGAGGGT	GAGTACGTGT	CCTCCTC	TCTC	GAGGTGGACTACATGGACGTC	

BASE NOS 541-600

[illegible]

Table 1
BASE NOS 541-600

M38.txt	SEQ ID NO 169	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT	550	560	570	580	590	600
M39.txt	SEQ ID NO 170	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M40.txt	SEQ ID NO 171	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M41.txt	SEQ ID NO 172	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M42.txt	SEQ ID NO 173	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M43.txt	SEQ ID NO 174	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M44.txt	SEQ ID NO 175	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M45.txt	SEQ ID NO 176	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M46.txt	SEQ ID NO 177	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M47.txt	SEQ ID NO 178	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M48 (Mav6).txt	SEQ ID NO 179	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M49.txt	SEQ ID NO 180	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						
M56 (Mav4).txt	SEQ ID NO 181	CGCCCGGCCAAGATGGTGTTCGGTGGCCACCGCGATGAT						

Table 1

BASE NOS 600-660

ATCC9-Mtb.txt	SEQ ID NO 1	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY621.txt	SEQ ID NO 2	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
Atcc1-av.txt	SEQ ID NO 3	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M29.txt	SEQ ID NO 4	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M30.txt	SEQ ID NO 5	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M31.txt	SEQ ID NO 6	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M32.txt	SEQ ID NO 7	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M33.txt	SEQ ID NO 8	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M34.txt	SEQ ID NO 9	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M48-new.txt	SEQ ID NO 10	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M49.txt	SEQ ID NO 11	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M64 (Mav2).txt	SEQ ID NO 12	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M65 (Mav3).txt	SEQ ID NO 13	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M67 (Mav5).txt	SEQ ID NO 14	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M69 (Mav7).txt	SEQ ID NO 15	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M71 (Mav9).txt	SEQ ID NO 16	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M91.txt	SEQ ID NO 17	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M94.txt	SEQ ID NO 18	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M95.txt	SEQ ID NO 19	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M96.txt	SEQ ID NO 20	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M100.txt	SEQ ID NO 21	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M101.txt	SEQ ID NO 22	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M102.txt	SEQ ID NO 23	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M104.txt	SEQ ID NO 24	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M105.txt	SEQ ID NO 25	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M106.txt	SEQ ID NO 26	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY111.txt	SEQ ID NO 27	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M76.txt	SEQ ID NO 28	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY451.txt	SEQ ID NO 29	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
ATCC2-chelnew.txt	SEQ ID NO 30	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M10.txt	SEQ ID NO 31	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M11-662.txt	SEQ ID NO 32	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M12.txt	SEQ ID NO 33	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M13 2 662.txt	SEQ ID NO 34	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M14.txt	SEQ ID NO 35	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M15.txt	SEQ ID NO 36	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M16.txt	SEQ ID NO 37	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M17 2 662.txt	SEQ ID NO 38	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M50.txt	SEQ ID NO 39	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M51.txt	SEQ ID NO 40	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M115.txt	SEQ ID NO 41	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M116.txt	SEQ ID NO 42	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M119.txt	SEQ ID NO 43	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY109.txt	SEQ ID NO 44	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY200.txt	SEQ ID NO 45	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY207.txt	SEQ ID NO 46	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MY209.txt	SEQ ID NO 47	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M122.txt	SEQ ID NO 48	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M123.txt	SEQ ID NO 49	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M124.txt	SEQ ID NO 50	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
Atcc3-for.txt	SEQ ID NO 51	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M53.txt	SEQ ID NO 52	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M54.txt	SEQ ID NO 53	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M55.txt	SEQ ID NO 54	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
M56.txt	SEQ ID NO 55	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG
MYA(May12).txt	SEQ ID NO 56	CAAACCGTGGCCCTCATGGGGGCAAA	CAATGCAGCGCCAGGCGGTG	CCGCTGGTCCGTAGCG

Table 1

M77.txt	SEQ_ID.NO.57
M118.txt	SEQ_ID.NO.58
MY221.txt	SEQ_ID.NO.59
MY223.txt	SEQ_ID.NO.60
MY225.txt	SEQ_ID.NO.61
My341.txt	SEQ_ID.NO.62
My715.txt	SEQ_ID.NO.63
MY470.txt	SEQ_ID.NO.64
Atcc4-go.txt	SEQ_ID.NO.65
ATCC4-0-Gord.txt	SEQ_ID.NO.66
M78(1s).txt	SEQ_ID.NO.67
M79(jd).txt	SEQ_ID.NO.68
M80(1g).txt	SEQ_ID.NO.69
M81(1l).txt	SEQ_ID.NO.70
M82(1m).txt	SEQ_ID.NO.71
M83(mb).txt	SEQ_ID.NO.72
M84(ow).txt	SEQ_ID.NO.73
M85(1b).txt	SEQ_ID.NO.74
M86(rb).txt	SEQ_ID.NO.75
M87(wm).txt	SEQ_ID.NO.76
MY90(gordDB).txt	SEQ_ID.NO.77
m126.txt	SEQ_ID.NO.78
m128.txt	SEQ_ID.NO.79
MY103.txt	SEQ_ID.NO.80
MY175.txt	SEQ_ID.NO.81
MY476.txt	SEQ_ID.NO.82
MY830.txt	SEQ_ID.NO.83
Atcc5-Int.txt	SEQ_ID.NO.84
Atcc5-0Int.txt	SEQ_ID.NO.85
M18.txt	SEQ_ID.NO.86
M19.txt	SEQ_ID.NO.87
M20.txt	SEQ_ID.NO.88
M21.txt	SEQ_ID.NO.89
M22.txt	SEQ_ID.NO.90
M23.txt	SEQ_ID.NO.91
M24.txt	SEQ_ID.NO.92
M25.txt	SEQ_ID.NO.93
M26.txt	SEQ_ID.NO.94
M27.txt	SEQ_ID.NO.95
M28.txt	SEQ_ID.NO.96
M107.txt	SEQ_ID.NO.97
MY107.txt	SEQ_ID.NO.98
MY112.txt	SEQ_ID.NO.99
MY312.txt	SEQ_ID.NO.100
Atcc6-kan.txt	SEQ_ID.NO.101
ATCC6-0Kan.txt	SEQ_ID.NO.102
M1.txt	SEQ_ID.NO.103
M2.txt	SEQ_ID.NO.104
M3.txt	SEQ_ID.NO.105
M4.txt	SEQ_ID.NO.106
M6.txt	SEQ_ID.NO.107
M7.txt	SEQ_ID.NO.108
M9.txt	SEQ_ID.NO.109
M57.txt	SEQ_ID.NO.110
M58.txt	SEQ_ID.NO.111
M59.txt	SEQ_ID.NO.112

[illegible]

Table 1

[illegible]

Table 1

SEQ ID NO 169	M38. txt
SEQ ID NO 170	M39. txt
SEQ ID NO 171	M40. txt
SEQ ID NO 172	M41. txt
SEQ ID NO 173	M42. txt
SEQ ID NO 174	M43. txt
SEQ ID NO 175	M44. txt
SEQ ID NO 176	M45. txt
SEQ ID NO 177	M46. txt
SEQ ID NO 178	M47. txt
SEQ ID NO 179	M68 (Mav6) . txt
SEQ ID NO 180	M89. txt
SEQ ID NO 181	M66 (Mav4) . txt

BASE NOS 660-720

[illegible]

Table 1

BASE NOS 660-720

M77.txt	SEQ ID NO 57	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M118.txt	SEQ ID NO 58	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY221.txt	SEQ ID NO 59	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY223.txt	SEQ ID NO 60	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY225.txt	SEQ ID NO 61	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY341.txt	SEQ ID NO 62	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY715.txt	SEQ ID NO 63	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY470.txt	SEQ ID NO 64	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
Atcc4-go.txt	SEQ ID NO 65	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
ATCC4-0-Gord.txt	SEQ ID NO 66	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M78(1z).txt	SEQ ID NO 67	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M79(jd).txt	SEQ ID NO 68	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M80(lg).txt	SEQ ID NO 69	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M81(11).txt	SEQ ID NO 70	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M82(rn).txt	SEQ ID NO 71	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M83(mb).txt	SEQ ID NO 72	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M84(ow).txt	SEQ ID NO 73	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M85(lb).txt	SEQ ID NO 74	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M86(rb).txt	SEQ ID NO 75	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M87(wi).txt	SEQ ID NO 76	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M90(gordDB).txt	SEQ ID NO 77	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
m126.txt	SEQ ID NO 78	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M128.txt	SEQ ID NO 79	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY103.txt	SEQ ID NO 80	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY475.txt	SEQ ID NO 81	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY476.txt	SEQ ID NO 82	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY830.txt	SEQ ID NO 83	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
Atcc5-int.txt	SEQ ID NO 84	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
ATCC5-0int.txt	SEQ ID NO 85	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M18.txt	SEQ ID NO 86	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M19.txt	SEQ ID NO 87	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M20.txt	SEQ ID NO 88	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M21.txt	SEQ ID NO 89	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M22.txt	SEQ ID NO 90	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M23.txt	SEQ ID NO 91	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M24.txt	SEQ ID NO 92	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M25.txt	SEQ ID NO 93	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M26.txt	SEQ ID NO 94	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M27.txt	SEQ ID NO 95	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M28.txt	SEQ ID NO 96	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY107.txt	SEQ ID NO 97	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY107.txt	SEQ ID NO 98	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY112.txt	SEQ ID NO 99	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY312.txt	SEQ ID NO 100	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
Atcc6-kan.txt	SEQ ID NO 101	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
ATCC6-0Kan.txt	SEQ ID NO 102	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M1.txt	SEQ ID NO 103	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M2.txt	SEQ ID NO 104	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M3.txt	SEQ ID NO 105	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M4.txt	SEQ ID NO 106	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M6.txt	SEQ ID NO 107	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M7.txt	SEQ ID NO 108	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M9.txt	SEQ ID NO 109	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M57.txt	SEQ ID NO 110	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
M58.txt	SEQ ID NO 111	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT
MY107.txt	SEQ ID NO 112	AGGCCCGGCTGGTGGGACCGGATGGAGCTGCGCGCGGCGGATCGACGCGGCGACGCT

Table 1
BASE NOS 660-720

M38. txt	SEQ ID NO 169	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	670
M39. txt	SEQ ID NO 170	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	680
M40. txt	SEQ ID NO 171	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	690
M41. txt	SEQ ID NO 172	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	700
M42. txt	SEQ ID NO 173	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	710
M43. txt	SEQ ID NO 174	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	720
M44. txt	SEQ ID NO 175	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M45. txt	SEQ ID NO 176	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M46. txt	SEQ ID NO 177	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M47. txt	SEQ ID NO 178	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M68(Mav6). txt	SEQ ID NO 179	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M89. txt	SEQ ID NO 180	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	
M66(Mav4). txt	SEQ ID NO 181	AGGC	CCGCTGGTGGGCA	CCGGGATGGA	TGCGCGCGGCGATCGACGCGGCGGACCGT	

Table 2

Afly#	SAMPLE ID#	Alt. ID	SPECIES
MY621		ATCC	<i>M. abscessus</i>
ATCC1	25291	ATCC-av	<i>M. avium</i>
M100	60300	MAC	<i>M. avium</i>
M101	60112	MAC	<i>M. avium</i>
M102	60268	MAC	<i>M. avium</i>
M103	60270	MAC	<i>M. avium</i>
M104	60272	MAC	<i>M. avium</i>
M105	60293	MAC	<i>M. avium</i>
M106	60313	MAC	<i>M. avium</i>
M107	60345	MAC	<i>M. avium</i>
M29	95-1784		<i>M. avium</i>
M30	95-1786		<i>M. avium</i>
M31	95-1788		<i>M. avium</i>
M32	95-1770		<i>M. avium</i>
M33	95-1775		<i>M. avium</i>
M34	95-1776		<i>M. avium</i>
M48	95-1765		<i>M. avium</i>
M49	95-1769		<i>M. avium</i>
M63	MAC #1	MAC	<i>M. avium</i>
M64	MAC #2	MAC	<i>M. avium</i>
M65	MAC #3	MAC	<i>M. avium</i>
M67	MAC #5	MAC	<i>M. avium</i>
M69	MAC #7	MAC	<i>M. avium</i>
M70	MAC #8	MAC	<i>M. avium</i>
M71	MAC #9	MAC	<i>M. avium</i>
M72	MAC #10	MAC	<i>M. avium</i>
M91	FM	<i>avium-intracell. FM(MAC)</i>	<i>M. avium</i>
M92	60040	MAC	<i>M. avium</i>
M93	60042	MAC	<i>M. avium</i>
M94	60049	MAC	<i>M. avium</i>
M95	60051	MAC	<i>M. avium</i>
M96	60110	MAC	<i>M. avium</i>
M97	60116	MAC	<i>M. avium</i>
M98	60123	MAC	<i>M. avium</i>
M99	60176	MAC	<i>M. avium</i>
M76	92-773		<i>M. bovis</i>
MY451			<i>M. bovis</i>
ATCC2	35752	ATCC-chel(new)	<i>M. chelonae</i>
M10	95A8151		<i>M. chelonae</i>
M11	95A0477		<i>M. chelonae</i>
M115	60121		<i>M. chelonae</i>
M116	52942		<i>M. chelonae</i>
M117	43192		<i>M. chelonae</i>
M118	53160		<i>M. chelonae</i>
M119	53131		<i>M. chelonae</i>
M12	95A4883		<i>M. chelonae</i>
M120	52923		<i>M. chelonae</i>
M121	52919		<i>M. chelonae</i>
M13	95A2611		<i>M. chelonae</i>
M14	95A0779		<i>M. chelonae</i>
M15	95A8654		<i>M. chelonae</i>
M16	95A8882		<i>M. chelonae</i>
M17	95A8881		<i>M. chelonae</i>
M50	95A11814		<i>M. chelonae</i>
M51	95A1102		<i>M. chelonae</i>
M75	#13	MAC#13	<i>M. chelonae</i>
MY109			<i>M. chelonae</i>
MY200			<i>M. chelonae</i>

Table 2

MY207			<i>M. chelonae</i>
MY209			<i>M. chelonae</i>
M122	60025		<i>M. flavescentis</i>
M123	60078		<i>M. flavescentis</i>
M124	60252		<i>M. flavescentis</i>
ATCC3	6841	ATCC-for	<i>M. fortuitum</i>
M53	60305		<i>M. fortuitum</i>
M54	60344		<i>M. fortuitum</i>
M55	60435		<i>M. fortuitum</i>
M56	60447		<i>M. fortuitum</i>
M74	#12	MAC#12	<i>M. fortuitum</i>
M88	CH	fort. CH	<i>M. fortuitum</i>
MY221			<i>M. fortuitum</i>
MY223			<i>M. fortuitum</i>
MY225			<i>M. fortuitum</i>
MY341			<i>M. fortuitum</i>
MY715			<i>M. fortuitum</i>
MY470			<i>M. genevieve</i>
ATCC4	14470	ATCC-go	<i>M. gordonae</i>
ATCC4-0		gord.	<i>M. gordonae</i>
M125	60068		<i>M. gordonae</i>
M126	60182		<i>M. gordonae</i>
M127	60214		<i>M. gordonae</i>
M128	60283		<i>M. gordonae</i>
M78	92-842	gord. LZ	<i>M. gordonae</i>
M79	93-692	gord. JD	<i>M. gordonae</i>
M80	94-94	gord. LG	<i>M. gordonae</i>
M81	93-1231	gord. LL	<i>M. gordonae</i>
M82	93-463	gord. RM	<i>M. gordonae</i>
M83	92-1219	gord. MB	<i>M. gordonae</i>
M84	91-1131	gord. OW	<i>M. gordonae</i>
M85	91-1478	gord. LB	<i>M. gordonae</i>
M86	92-642	gord. RB	<i>M. gordonae</i>
M87	93-1180	gord. WN	<i>M. gordonae</i>
M90	DB	gord. DB	<i>M. gordonae</i>
MY103			<i>M. gordonae</i>
MY475			<i>M. gordonae</i>
MY476			<i>M. gordonae</i>
MY746			<i>M. gordonae</i>
MY830			<i>M. gordonae</i>
ATCC5		ATCC-int	<i>M. intracellulare</i>
ATCC5-0		intra	<i>M. intracellulare</i>
M18	95-1778		<i>M. intracellulare</i>
M19	95-1780		<i>M. intracellulare</i>
M20	95-1781		<i>M. intracellulare</i>
M21	95-1782		<i>M. intracellulare</i>
M22	95-1790		<i>M. intracellulare</i>
M23	95-1794		<i>M. intracellulare</i>
M24	95-1796		<i>M. intracellulare</i>
M25	95-1777		<i>M. intracellulare</i>
M26	95-1779		<i>M. intracellulare</i>
M27	95-1780		<i>M. intracellulare</i>
M28	95-1781		<i>M. intracellulare</i>
ATCC6	12478	ATCC-kan	<i>M. kansasii</i>
ATCC6-0		kan.	<i>M. kansasii</i>
M1	95A5375		<i>M. kansasii</i>
M2	95A10299		<i>M. kansasii</i>
M3	96A0020		<i>M. kansasii</i>
M4	95A3977		<i>M. kansasii</i>

Table 2

M5	95A4739		<i>M. kansasii</i>
M52	95A5381		<i>M. kansasii</i>
M57	60183		<i>M. kansasii</i>
M58	60180		<i>M. kansasii</i>
M59	60207		<i>M. kansasii</i>
M6	95A2685		<i>M. kansasii</i>
M60	60284		<i>M. kansasii</i>
M61	60308		<i>M. kansasii</i>
M62	60314		<i>M. kansasii</i>
M7	95A2694		<i>M. kansasii</i>
M73	#11	MAC#11	<i>M. kansasii</i>
M8	94A8042		<i>M. kansasii</i>
M9	95A1275		<i>M. kansasii</i>
MY106			<i>M. kansasii</i>
MY141			<i>M. kansasii</i>
MY216			<i>M. kansasii</i>
MY218			<i>M. kansasii</i>
MY228			<i>M. kansasii</i>
M108	60044		<i>M. malmoense</i>
M109	60149		<i>M. malmoense</i>
M110	60211		<i>M. malmoense</i>
M111	60202		<i>M. malmoense</i>
M112	60085		<i>M. malmoense</i>
M113	60047		<i>M. malmoense</i>
M114	60185		<i>M. malmoense</i>
MY325		ATCC	<i>M. malmoense</i>
MY718		malmo	<i>M. malmoense</i>
MY214			<i>M. marinum</i>
MY224			<i>M. marinum</i>
MY244			<i>M. marinum</i>
MY339			<i>M. marinum</i>
MY343			<i>M. marinum</i>
MY458		ATCC	<i>M. mucogenicum</i>
MY809			<i>M. mucogenicum</i>
MY817			<i>M. mucogenicum</i>
MY821			<i>M. mucogenicum</i>
MY824			<i>M. mucogenicum</i>
MY102			<i>M. nonchromogenicum</i>
MY105			<i>M. nonchromogenicum</i>
MY251			<i>M. nonchromogenicum</i>
MY258			<i>M. nonchromogenicum</i>
MY294			<i>M. nonchromogenicum</i>
ATCC7	19981	ATCC-ecr	<i>M. scrofulaceum</i>
ATCC7-0		scrof.	<i>M. scrofulaceum</i>
MY121			<i>M. scrofulaceum</i>
MY249			<i>M. scrofulaceum</i>
MY372			<i>M. scrofulaceum</i>
MY378			<i>M. scrofulaceum</i>
MY484			<i>M. simiae</i>
MY556			<i>M. simiae</i>
MY563			<i>M. simiae</i>
MY586			<i>M. simiae</i>
ATCC8	19420	ATCC-sma	<i>M. smegmatis</i>
M35	95A1072		<i>M. smegmatis</i>
M36	95A8183		<i>M. smegmatis</i>
M37	95A4980		<i>M. smegmatis</i>
M77	82-144	smeg. JL	<i>M. smegmatis</i>
MY143		ATCC	<i>M. smegmatis</i>
MY104			<i>M. szulgai</i>

Table 2

MY196			<i>M. szulgai</i>
MY357			<i>M. szulgai</i>
MY358			<i>M. szulgai</i>
MY480			<i>M. szulgai</i>
TB74	C.17.96.5		<i>M. tb</i> M160 DR
MY387			<i>M. tb</i>
MY418			<i>M. tb</i>
MY437			<i>M. tb</i>
MY482			<i>M. tb</i>
TB59	C.18.96.1		<i>M. tb</i> H37rv DR
TB67	C.18.96.1		<i>M. tb</i> H37rv DR
TB73	C.17.96.1		<i>M. tb</i> H37rv DR
TB60	C.18.96.2		<i>M. tb</i> J35 DR
TB65	C.22.96.6		<i>M. tb</i> M101 DR
TB62	C.18.96.4		<i>M. tb</i> M104 DR
TB69	C.18.96.3		<i>M. tb</i> M104 DR
TB72	C.18.96.7		<i>M. tb</i> M104DR
TB68	C.22.96.10		<i>M. tb</i> M112 DR
TB83	C.18.96.5		<i>M. tb</i> M140 DR
TB64	C.18.96.6		<i>M. tb</i> M160 DR
TB70	C.18.96.4		<i>M. tb</i> M160 DR
TB81	C.18.96.3		<i>M. tb</i> M60 DR
TB68	C.18.96.2		<i>M. tb</i> M60 DR
TB71	C.18.96.6		<i>M. tb</i> M60 DR
MY212			<i>M. terrae</i>
MY354			<i>M. terrae</i>
MY491			<i>M. terrae</i>
MY497			<i>M. terrae</i>
MY816			<i>M. triplex</i>
ATCC9	27294	Mtb	<i>M. tuberculosis</i>
ATCC9-0		TB2020	<i>M. tuberculosis</i>
N/A	93-1071		<i>M. tuberculosis</i>
N/A	93-338		<i>M. tuberculosis</i>
N/A	92-852		<i>M. tuberculosis</i>
N/A	92-1005		<i>M. tuberculosis</i>
N/A	92-243		<i>M. tuberculosis</i>
N/A	92-304		<i>M. tuberculosis</i>
N/A	92-199		<i>M. tuberculosis</i>
N/A	92-197		<i>M. tuberculosis</i>
N/A	92-484		<i>M. tuberculosis</i>
N/A	94-577		<i>M. tuberculosis</i>
TB1	936		<i>M. tuberculosis</i>
TB10	1122		<i>M. tuberculosis</i>
TB11	3407		<i>M. tuberculosis</i>
TB12	978		<i>M. tuberculosis</i>
TB13	3553		<i>M. tuberculosis</i>
TB14	3466		<i>M. tuberculosis</i>
TB15	2163		<i>M. tuberculosis</i>
TB16	DW	DW	<i>M. tuberculosis</i>
TB17	CB	CB	<i>M. tuberculosis</i>
TB18	PB	PB	<i>M. tuberculosis</i>
TB19	AA	AA	<i>M. tuberculosis</i>
TB2	M0404A		<i>M. tuberculosis</i>
TB20	3492		<i>M. tuberculosis</i>
TB21	1435		<i>M. tuberculosis</i>
TB22	696		<i>M. tuberculosis</i>
TB23	2268		<i>M. tuberculosis</i>
TB24	3455		<i>M. tuberculosis</i>
TB25	37		<i>M. tuberculosis</i>

Table 2

TB26	173		<i>M. tuberculosis</i>
TB27	230		<i>M. tuberculosis</i>
TB28	2519		<i>M. tuberculosis</i>
TB29	T29233		<i>M. tuberculosis</i>
TB3	1231		<i>M. tuberculosis</i>
TB30	SP	SP	<i>M. tuberculosis</i>
TB31	3201		<i>M. tuberculosis</i>
TB32	3219		<i>M. tuberculosis</i>
TB33	60		<i>M. tuberculosis</i>
TB34	3442		<i>M. tuberculosis</i>
TB35	3502		<i>M. tuberculosis</i>
TB36	3759		<i>M. tuberculosis</i>
TB37	1295		<i>M. tuberculosis</i>
TB38	337		<i>M. tuberculosis</i>
TB39	384		<i>M. tuberculosis</i>
TB4	914		<i>M. tuberculosis</i>
TB40	499		<i>M. tuberculosis</i>
TB41	535		<i>M. tuberculosis</i>
TB42	607		<i>M. tuberculosis</i>
TB43	707		<i>M. tuberculosis</i>
TB44	692		<i>M. tuberculosis</i>
TB45	2408		<i>M. tuberculosis</i>
TB46	1069		<i>M. tuberculosis</i>
TB47	M3262A		<i>M. tuberculosis</i>
TB48	1336		<i>M. tuberculosis</i>
TB49	1388		<i>M. tuberculosis</i>
TB5	1145		<i>M. tuberculosis</i>
TB50	65		<i>M. tuberculosis</i>
TB51	727		<i>M. tuberculosis</i>
TB52	3465		<i>M. tuberculosis</i>
TB53	3506		<i>M. tuberculosis</i>
TB54	9600367		<i>M. tuberculosis</i>
TB55	9600173		<i>M. tuberculosis</i>
TB56	9503471		<i>M. tuberculosis</i>
TB57	9600309		<i>M. tuberculosis</i>
TB58	9600230		<i>M. tuberculosis</i>
TB6	1417		<i>M. tuberculosis</i>
TB7	SM2341		<i>M. tuberculosis</i>
TB75	2096		<i>M. tuberculosis</i>
TB76	173/1		<i>M. tuberculosis</i>
TB77	1122/1		<i>M. tuberculosis</i>
TB78	1417/1		<i>M. tuberculosis</i>
TB8	1567		<i>M. tuberculosis</i>
TB9	M7032A		<i>M. tuberculosis</i>
ATCC10	19250	ATCC-xen	<i>M. xenopi</i>
M129	60133		<i>M. xenopi</i>
M130	60200		<i>M. xenopi</i>
M131	60365		<i>M. xenopi</i>
M132	60367		<i>M. xenopi</i>
M38	95A5208		<i>M. xenopi</i>
M39	95A5399		<i>M. xenopi</i>
M40	95A3938		<i>M. xenopi</i>
M41	95A6782		<i>M. xenopi</i>
M42	95A0933		<i>M. xenopi</i>
M43	95A4320		<i>M. xenopi</i>
M44	95A3478		<i>M. xenopi</i>
M45	95A2997		<i>M. xenopi</i>
M46	95A8383		<i>M. xenopi</i>
M47	95A4319		<i>M. xenopi</i>

Table 2

M68	MAC #8	MAC #8	<i>M. xenopi</i>
M89	SG	xen. SG	<i>M. xenopi</i>
MY219			<i>M. xenopi</i>
MY250			<i>M. xenopi</i>
MY252			<i>M. xenopi</i>
MY254			<i>M. xenopi</i>
MY255			<i>M. xenopi</i>
MY107			MAC
MY111			MAC
MY112			MAC
MY312			MAC
M68	MAC #4	MAC #4	unique